

11



1638

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/508,377

DATE: 03/18/2002

TIME: 14:17:04

Input Set : N:\Crf3\Refhold\I508377.raw

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1 <110> APPLICANT: KALEEN, ZHONGYILI
 2 MORELL, MATTHEW
 3 RAHMAN, SADEQUR
 4 <120> TITLE OF INVENTION: REGULATION OF GENE EXPRESSION IN PLANTS
 5 <130> FILE REFERENCE: 054270/0126
 6 <140> CURRENT APPLICATION NUMBER: US/09/508,377
 7 <141> CURRENT FILING DATE: 2000-06-09
 8 <150> PRIOR APPLICATION NUMBER: AU PP 2509
 9 <151> PRIOR FILING DATE: 1998-03-20
 10 <150> PRIOR APPLICATION NUMBER: PCT/AU98/00743
 11 <151> PRIOR FILING DATE: 1998-09-11
 12 <150> PRIOR APPLICATION NUMBER: AU PP 9108
 13 <151> PRIOR FILING DATE: 1997-09-12
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 20 <213> ORGANISM: Artificial Sequence
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 22 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 23 <221> NAME/KEY: modified_base
 24 <222> LOCATION: (4)
 25 <223> OTHER INFORMATION: a, t, c, g, other or unknown
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 30 <222> LOCATION: (10)
 31 <223> OTHER INFORMATION: a, t, c, g, other or unknown
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 36 <211> LENGTH: 19
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 38 <213> ORGANISM: Artificial Sequence
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 40 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 41 <400> SEQUENCE: 2
 42 tacatttcoct tgtccatca 19
 44 <210> SEQ ID NO: 3
 45 <211> LENGTH: 18
 46 <212> TYPE: DNA

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56 <213> ORGANISM: Artificial Sequence
57 <220> FEATURE:
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63 <211> LENGTH: 2687
64 <212> TYPE: DNA
65 <213> ORGANISM: Triticum tauschii
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69      tcccgtgtct gcgccaagag actacaccat ggcaacagct gaagatggtg ttggcgacct 180
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92      gaccaacagg agatatacgg aaaagtgcac tgcataatgt gagagccacg atcagtctat 1560
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94      agacttgcat cctgcttcac ctacaattga tcgtggaatt gcacttcaaa agatgattca 1680
95      cttcacacac atggcccttg gaggtgatgg ctacttgaat tttatgggta atgagtttgg 1740
96      ccacccagaa tggattgact ttccaagaga aggcaacaac tggagttatg ataaatgcag 1800
97      acgccagtgg agcctctcag acattgatca cctacgatac aagtacatga acgcatttga 1860

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98      tcaagcaatg aatgcgctcg acgacaagtt ttccttctcta tcgtcatcaa agcagattgt 1920
99      cagcgacatg aatgaggaaa agaagattat tgtatttgaa cgtggagatc tggctctcgt 1980
100     cttcaatttt catcccagta aaacttatga tggttacaaa gtcggatgtg atttgctgg 2040
101     gaagtacaag gtagctctgg actccgatgc tctgatgttt ggtggacatg gaagagtggc 2100
102     ccagtacaac gatcacttca cgtcacctga aggagtacca ggagtacctg aaacaaactt 2160
103     caacaaccgc cctaattcat tcaaagtcct gtctccaccc cgcacttggtg tggcttacta 2220
104     tcgcgtcgag gaaaaagcgg aaaagcctaa ggatgaagga gctgcttctt ggggcaaagc 2280
105     tgctcctggg tacatcgatg ttgaagccac tcgtgtcaaa gacgcagcag atggtgaggc 2340
106     gacttctggt tccaaaaagg cgtctacagg aggtgactcc agcaagaagg gaattaactt 2400
107     tgtcttcggg tcacctgaca aagataacaa ataagcacca tatcaacgct tgatcagaac 2460
108     cgtgtaccga cgtccttgta atattcctgc tattgctagt agtagcaata ctgtcaaact 2520
109     gtgcagactt gagattctgg cttggacttt gctgaggtta cctactatat agaaagataa 2580
110     ataagaggtg atggtgcggg tcgagtcggg ctatatgtgc caaatatgcg ccatcccag 2640
111     tcctctgtca taaaggaagt ttcgggcttt cagcccagaa taaaaaa 2687
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115 <212> TYPE: PRT
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122      Ser Lys Phe Ser Val Pro Val Ser Ala Pro Arg Asp Tyr Thr Met Ala
123      35          40          45
124      Thr Ala Glu Asp Gly Val Gly Asp Leu Pro Ile Tyr Asp Leu Asp Pro
125      50          55          60
126      Lys Phe Ala Gly Phe Lys Glu His Phe Ser Tyr Arg Met Lys Lys Tyr
127      65          70          75          80
128      Leu Asp Gln Lys His Ser Ile Glu Lys His Glu Gly Gly Leu Glu Glu
129      85          90          95
130      Phe Ser Lys Gly Tyr Leu Lys Phe Gly Ile Asn Thr Glu Asn Asp Ala
131      100         105         110
132      Thr Val Tyr Arg Glu Trp Ala Pro Ala Ala Met Asp Ala Gln Leu Ile
133      115         120         125
134      Gly Asp Phe Asn Asn Trp Asn Gly Ser Gly His Arg Met Thr Lys Asp
135      130         135         140
136      Asn Tyr Gly Val Trp Ser Ile Arg Ile Ser His Val Asn Gly Lys Pro
137      145         150         155         160
138      Ala Ile Pro His Asn Ser Lys Val Lys Phe Arg Phe His Arg Gly Asp
139      165         170         175
140      Gly Leu Trp Val Asp Arg Val Pro Ala Trp Ile Arg Tyr Ala Thr Phe
141      180         185         190
142      Asp Ala Ser Lys Phe Gly Ala Pro Tyr Asp Gly Val His Trp Asp Pro
143      195         200         205
144      Pro Ser Gly Glu Arg Tyr Val Phe Lys His Pro Arg Pro Arg Lys Pro
145      210         215         220
146      Asp Ala Pro Arg Ile Tyr Glu Ala His Val Gly Met Ser Gly Glu Arg
147      225         230         235         240

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148   Pro Glu Val Ser Thr Tyr Arg Glu Phe Ala Asp Asn Val Leu Pro Arg
149           245                               250           255
150   Ile Lys Ala Asn Asn Tyr Asn Thr Val Gln Leu Met Ala Ile Met Glu
151           260                               265           270
152   His Ser Ile Leu Cys Phe Phe Trp Tyr His Val Thr Asn Phe Phe Ala
153           275                               280           285
154   Val Ser Ser Arg Ser Gly Thr Pro Glu Asp Leu Lys Tyr Leu Val Asp
155           290                               295           300
156   Lys Ala His Ser Leu Gly Leu Arg Val Leu Met Asp Val Val His Ser
157           305                               310           315           320
158   His Ala Ser Ser Asn Met Thr Asp Gly Leu Asn Gly Tyr Asp Val Gly
159           325                               330           335
160   Gln Asn Thr Gln Glu Ser Tyr Phe His Thr Gly Glu Arg Gly Tyr His
161           340                               345           350
162   Lys Leu Trp Asp Ser Arg Leu Phe Asn Tyr Ala Asn Trp Glu Val Leu
163           355                               360           365
164   Arg Tyr Leu Leu Ser Asn Leu Arg Tyr Trp Met Asp Glu Phe Met Phe
165           370                               375           380
166   Asp Gly Phe Arg Phe Asp Gly Val Thr Ser Met Leu Tyr Asn His His
167           385                               390           395           400
168   Gly Ile Asn Met Ser Phe Ala Gly Asn Tyr Lys Glu Tyr Phe Gly Leu
169           405                               410           415
170   Asp Thr Asp Val Asp Ala Val Val Tyr Met Met Leu Ala Asn His Leu
171           420                               425           430
172   Met His Lys Ile Leu Pro Glu Ala Thr Val Val Ala Glu Asp Val Ser
173           435                               440           445
174   Gly Met Pro Val Leu Cys Arg Ser Val Asp Glu Gly Gly Val Gly Phe
175           450                               455           460
176   Asp Tyr Arg Leu Ala Met Ala Ile Pro Asp Arg Trp Ile Asp Tyr Leu
177           465                               470           475           480
178   Lys Asn Lys Asp Asp Leu Glu Trp Ser Met Ser Ala Ile Ala His Thr
179           485                               490           495
180   Leu Thr Asn Arg Arg Tyr Thr Glu Lys Cys Ile Ala Tyr Ala Glu Ser
181           500                               505           510
182   His Asp Gln Ser Ile Val Gly Asp Lys Thr Met Ala Phe Leu Leu Met
183           515                               520           525
184   Asp Lys Glu Met Tyr Thr Gly Met Ser Asp Leu Gln Pro Ala Ser Pro
185           530                               535           540
186   Thr Ile Asp Arg Gly Ile Ala Leu Gln Lys Met Ile His Phe Ile Thr
187           545                               550           555           560
188   Met Ala Leu Gly Gly Asp Gly Tyr Leu Asn Phe Met Gly Asn Glu Phe
189           565                               570           575
190   Gly His Pro Glu Trp Ile Asp Phe Pro Arg Glu Gly Asn Asn Trp Ser
191           580                               585           590
192   Tyr Asp Lys Cys Arg Arg Gln Trp Ser Leu Ser Asp Ile Asp His Leu
193           595                               600           605
194   Arg Tyr Lys Tyr Met Asn Ala Phe Asp Gln Ala Met Asn Ala Leu Asp
195           610                               615           620
196   Asp Lys Phe Ser Phe Leu Ser Ser Ser Lys Gln Ile Val Ser Asp Met

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197      625      630      635      640
198  Asn Glu Glu Lys Lys Ile Ile Val Phe Glu Arg Gly Asp Leu Val Phe
199      645      650      655
200  Val Phe Asn Phe His Pro Ser Lys Thr Tyr Asp Gly Tyr Lys Val Gly
201      660      665      670
202  Cys Asp Leu Pro Gly Lys Tyr Lys Val Ala Leu Asp Ser Asp Ala Leu
203      675      680      685
204  Met Phe Gly Gly His Gly Arg Val Ala Gln Tyr Asn Asp His Phe Thr
205      690      695      700
206  Ser Pro Glu Gly Val Pro Gly Val Pro Glu Thr Asn Phe Asn Asn Arg
207  705      710      715      720
208  Pro Asn Ser Phe Lys Val Leu Ser Pro Pro Arg Thr Cys Val Ala Tyr
209      725      730      735
210  Tyr Arg Val Glu Glu Lys Ala Glu Lys Pro Lys Asp Glu Gly Ala Ala
211      740      745      750
212  Ser Trp Gly Lys Ala Ala Pro Gly Tyr Ile Asp Val Glu Ala Thr Arg
213      755      760      765
214  Val Lys Asp Ala Ala Asp Gly Glu Ala Thr Ser Gly Ser Lys Lys Ala
215      770      775      780
216  Ser Thr Gly Gly Asp Ser Ser Lys Lys Gly Ile Asn Phe Val Phe Gly
217  785      790      795      800
218  Ser Pro Asp Lys Asp Asn Lys
219      805
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222 <211> LENGTH: 319
223 <212> TYPE: DNA
224 <213> ORGANISM: Triticum tauschii
225 <400> SEQUENCE: 7
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227  tttgtcttcg ggtcacctga caaagataac aaataagcac catatcaacg cttgatcaga 120
228  accgtgtacc gacgtccttg taatattcct gctattgcta gtagtagcaa tactgtcaaa 180
229  ctgtgcagac ttgagattct ggcttggaact ttgctgaggt tacctactat atagaaagat 240
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231  agtcctctgt cataaagga 319
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234 <211> LENGTH: 4890
235 <212> TYPE: DNA
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240  ggctgcggct ttaaaggccg gccaggctga ggtgtccggg tcggacacgg cccgtaaggc 180
241  ggttgacttt aaaaaataat aattcggaca tgcaaaaaag taagaaaaga aataataaac 240
242  ggactccaaa aatcccgaag taaatttttc ccattctta aaaataagcc ggacaagatg 300
243  aacatttatt tgggcctaaa atgcaatttt gaaaaatgcg tatttttcct aattcggaat 360
244  aaaaatcaaat aaaatccaaa taaaatcaaa tatttgtttt taatattttt cctccaatat 420
245  ttcatatttt gtgaagaagt cattttatcc catctcatat attttgatat gaaatatttt 480
246  cggagagaaa aataattaaa acaaatgata ctattttcaa aatttgagaa aaccctaaata 540
247  tgaaaaataac gaaatcccca actctctccg tgggtccttg agttgcgtga aatttctagg 600

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VERIFICATION SUMMARY

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DATE: 03/18/2002

TIME: 14:17:05

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